SEQUENCE LISTING

```
<110> Zhou, Shibin
           Zawel, Leigh
           Vogelstein, Bert
           Kinzler, Kenneth
     <120> Human Fast-1 Gene
     <130> 01107.10898
     <140> 09/113,309
     <141> 1998-07-10
     <160> 19
     <170> FastSEO for Windows Version 3.0
     <210> 1
     <211> 1793
     <212> DNA
     <213> Homo sapiens
      <400> 1
gttgagtcaa tgtgtccccc tcttgttcct agggtgcggg cttcatggcc ttctcctcca
                                                                     60
ggaageteea cetgateatg teetgggtgg atateeagee eecatagtte agggeetact
                                                                    120
agcagetget agatettgaa etecaggage geeceaegee ttgggagett ggeatggget
                                                                    180
aaatactccc ccatttgtta aatggggtcc tgaaacctga ccagggaaga cgggataaag
                                                                    240
tagecatggg teategeage ceetttgaag cegggeetgg ceacceaaag geaacteagg
                                                                    300
ggtggagact gaggcctcag gagaaqcccc cactaqaatg etetetgecc etecetteca
                                                                    360
420
ttectecett cectecete eccettecat cegaatgata aaggeeccag eccgectgee
                                                                    480
ccagccegge ctcaggtccc ggccctgcct tctacactgc cccaccqccc tqcaccetcc
                                                                    540
accoggocag geocetgece acgetgteta cegtecegea tggggecetg cageggetee
                                                                    600
cgcctggggc ccccagaggc agagtcgccc tcccagcccc ctaagaggag gaagaagagg
                                                                     660
tacctgcgac atgacaagcc cccctacacc tacttggcca tgatcgcctt ggtgattcag
                                                                    720
geogetecet ecogeagact gaagetggee cagateatee gteaggteea ggeogtgtte
                                                                    780
cccttcttca gggaagacta cgagggctgg aaagactcca ttcgccacaa cctttcctcc
                                                                     840
aaccgatgct tccgcaaggt gcccaaggac cctgcaaagc cccaggccaa gggcaacttc
                                                                     900
tgggcggtcg acgtgagcct gatcccagct gaggcgctcc ggctgcagaa caccgccctg
                                                                     960
tgccggcgct ggcagaacgg aggtgcgcgt ggagccttcg ccaaggacct gggcccctac
                                                                   1020
gtgctgcacg gccggccata ccggccgccc agtcccccgc caccacccag tgagggcttc
                                                                   1080
agcatcaagt ccctgctagg agggtccggg gagggggcac cctggccggg gctagctcca
                                                                   1140
cagagcagcc cagtteetgc aggcacaggg aacagtgggg aggaggeggt geecacceca
                                                                   1200
ccccttccct cttctgagag gcctctgtgg cccctctgcc cccttcctgg ccccacgaga
                                                                   1260
gtggagggg agactgtgca ggggggagcc atcgggccct caaccetete eccagagcet
                                                                   1320
agggeetgge etetecaett aetgeaggge acegeagtte etgggggaeg gteeageggg
                                                                   1380
ggacacaggg cotcoctctg ggggcagetg cocacctcct acttgcctat ctacactccc
                                                                   1440
aatgtggtaa tgcccttggc accaccaccc acctcctgtc cccagtgtcc gtcaaccagc
                                                                   1500
cetgectact ggggggtggc ceetgaaacc cgagggeecc cagggetget etgegateta
                                                                   1560
gacgccctct tccaaggggt gccacccaac aaaagcatct acgacgtttg ggtcagccac
                                                                   1620
cetegggace tggeggecee tggeceagge tggetgetet cetggtgeag cetgtgagge
                                                                   1680
tettaagaca ggggccgctc ctccctcccg ctcccacccc caccttgttg acagggagca
                                                                   1740
agggaggegg etgtetgega cacageaget egaaaaceag geagagettg ttg
                                                                    1793
```

<210> 2 <211> 365 <212> PRT

<213> Homo sapiens

<400> 2 Met Gly Pro Cys Ser Gly Ser Arg Leu Gly Pro Pro Glu Ala Glu Ser 10 Pro Ser Gln Pro Pro Lys Arg Arg Lys Lys Arg Tyr Leu Arg His Asp 25 Lys Pro Pro Tyr Thr Tyr Leu Ala Met Ile Ala Leu Val Ile Gln Ala 40 Ala Pro Ser Arg Arg Leu Lys Leu Ala Gln Ile Ile Arg Gln Val Gln 55 Ala Val Phe Pro Phe Phe Arg Glu Asp Tyr Glu Gly Trp Lys Asp Ser 70 75 Ile Arq His Asn Leu Ser Ser Asn Arg Cys Phe Arg Lys Val Pro Lys 85 90 Asp Pro Ala Lys Pro Gln Ala Lys Gly Asn Phe Trp Ala Val Asp Val 105 Ser Leu Ile Pro Ala Glu Ala Leu Arg Leu Gln Asn Thr Ala Leu Cys 120 Arg Arg Trp Gln Asn Gly Gly Ala Arg Gly Ala Phe Ala Lys Asp Leu 135 Gly Pro Tyr Val Leu His Gly Arg Pro Tyr Arg Pro Pro Ser Pro Pro 150 155 Pro Pro Pro Ser Glu Gly Phe Ser Ile Lys Ser Leu Leu Gly Gly Ser 165 170 Gly Glu Gly Ala Pro Trp Pro Gly Leu Ala Pro Gln Ser Ser Pro Val 185 Pro Ala Gly Thr Gly Asn Ser Gly Glu Glu Ala Val Pro Thr Pro Pro 200 Leu Pro Ser Ser Glu Arg Pro Leu Trp Pro Leu Cys Pro Leu Pro Gly 215 Pro Thr Arg Val Glu Gly Glu Thr Val Gln Gly Gly Ala Ile Gly Pro 230 235 Ser Thr Leu Ser Pro Glu Pro Arg Ala Trp Pro Leu His Leu Leu Gln 245 250 Gly Thr Ala Val Pro Gly Gly Arg Ser Ser Gly Gly His Arg Ala Ser 265 260 Leu Trp Gly Gln Leu Pro Thr Ser Tyr Leu Pro Ile Tyr Thr Pro Asn 280 Val Val Met Pro Leu Ala Pro Pro Pro Thr Ser Cys Pro Gln Cys Pro 295 300 Ser Thr Ser Pro Ala Tyr Trp Gly Val Ala Pro Glu Thr Arg Gly Pro 310 315 Pro Gly Leu Leu Cys Asp Leu Asp Ala Leu Phe Gln Gly Val Pro Pro 325 330 Asn Lys Ser Ile Tyr Asp Val Trp Val Ser His Pro Arg Asp Leu Ala 345 Ala Pro Gly Pro Gly Trp Leu Leu Ser Trp Cys Ser Leu

355 <210> 3 <211> 477

<212> PRT

<213> Homo sapiens

<400> 3
Val Ala Met Ile Asn Ala Cys Ile Asp Ser Met Ser Ser Ile Leu Pro
1 5 10 15

360

Phe Thr Pro Pro Val Val Lys Arg Leu Leu Gly Trp Lys Lys Ser Ala 25 Gly Gly Ser Gly Gly Ala Gly Gly Gly Glu Gln Asn Gly Gln Glu Glu 40 Lys Trp Cys Glu Lys Ala Val Lys Ser Leu Val Lys Lys Leu Lys Lys 55 Thr Gly Arg Leu Asp Glu Leu Glu Lys Ala Ile Thr Thr Gln Asn Cys 70 75 Asn Thr Lys Cys Val Thr Ile Pro Ser Thr Cys Ser Glu Ile Trp Gly 90 85 Leu Ser Thr Pro Asn Thr Ile Asp Gln Trp Asp Thr Thr Gly Leu Tyr 100 105 Ser Phe Ser Glu Gln Thr Arg Ser Leu Asp Gly Arg Leu Gln Val Ser 120 125 His Arg Lys Gly Leu Pro His Val Ile Tyr Cys Arg Leu Trp Arg Trp 135 140 Pro Asp Leu His Ser His His Glu Leu Lys Ala Ile Glu Asn Cys Glu 150 155 Tyr Ala Phe Asn Leu Lys Lys Asp Glu Val Cys Val Asn Pro Tyr His 165 170 Tyr Gln Arg Val Glu Thr Pro Val Leu Pro Pro Val Leu Val Pro Arg 185 His Thr Glu Ile Leu Thr Glu Leu Pro Pro Leu Asp Asp Tyr Thr His 200 Ser Ile Pro Glu Asn Thr Asn Phe Pro Ala Gly Ile Glu Pro Gln Ser 215 Asn Tyr Ile Pro Glu Thr Pro Pro Pro Gly Tyr Ile Ser Glu Asp Gly 230 235 Glu Thr Ser Asp Gln Gln Leu Asn Gln Ser Met Asp Thr Gly Ser Pro 245 250 Ala Glu Leu Ser Pro Thr Thr Leu Ser Pro Val Asn His Ser Leu Asp 260 265 Leu Gln Pro Val Thr Tyr Ser Glu Pro Ala Phe Trp Cys Ser Ile Ala 280 Tyr Tyr Glu Leu Asn Gln Arg Val Gly Glu Thr Phe His Ala Ser Gln 295 300 Pro Ser Leu Thr Val Asp Gly Phe Thr Asp Pro Ser Asn Ser Glu Arg 315 310 Phe Cys Leu Gly Leu Leu Ser Asn Val Asn Arg Asn Ala Thr Val Glu 330 325 Met Thr Arg Arg His Ile Gly Arg Gly Val Arg Leu Tyr Tyr Ile Gly 340 345 350 Gly Glu Val Phe Ala Glu Cys Leu Ser Asp Ser Ala Ile Phe Val Gln 360 Ser Pro Asn Cys Asn Gln Arg Tyr Gly Trp His Pro Ala Thr Val Cys 375 380 Lys Ile Pro Pro Gly Cys Asn Leu Lys Ile Phe Asn Asn Gln Glu Phe 390 395 Ala Ala Leu Leu Ala Gln Ser Val Asn Gln Gly Phe Glu Ala Val Tyr 405 410 Gln Leu Thr Arg Met Cys Thr Ile Arg Met Ser Phe Val Lys Gly Trp 420 425 Gly Ala Glu Tyr Arg Arg Gln Thr Val Thr Ser Thr Pro Cys Trp Ile 435 440 Glu Leu His Leu Asn Gly Pro Leu Gln Trp Leu Asp Lys Val Leu Thr 455 Gln Met Gly Ser Pro Ser Val Arg Cys Ser Ser Met Ser 470

<210> 4	
<211> 8	
<212> DNA	
<213> Homo sapiens	
(213) NOMO Sapiens	
400	
<400> 4	
tgtkkatt	8
<210> 5	
<211> 18	
<212> DNA	
<213> Homo sapiens	
<400> 5	
ctggaaagac tccattcg	18
<210> 6	
<211> 19	
<212> DNA	
<213> Homo sapiens	
AZISF IIIIIII DALZISID	
<400> 6	
cacagaggcc tetcagaag	19
cacagaggee	19
210. 7	
<210> 7	
<211> 18	
<212> DNA	
<213> Homo sapiens	
<400> 7	
ccecettcea tecgaatg	18
<210> 8	
<211> 19	
<212> DNA	
<213> Homo sapiens	
<400> 8	
gagetgetgt gtegeagae	19
<210> 9	
<211> 79	
<212> DNA	
<213> Artificial Sequence	
The state of the s	
<220>	
<223> flag primer	
<223> IIad bilmer	
<400> 9	
ggatectaat acgaeteact atagggagae caccatggae tacaaggaeg acgatgacaa	60
ggggccctgc ageggetec	75
<210> 10	
<211> 81	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> flag primer	

<400> 10	
ggatectaat acgaeteaet atagggagae caccatggae tacaaggaeg acgatgaeaa	60
qcccttcct qqcccacga g	81
<210> 11	
<211> 31	
<212> DNA	
<213> Homo sapiens	
<213> nomo sapiens	
<400> 11	
tatgeggeeg ceaceatggg geeetgeage g	31
Latiguage of coaccatage g	31
<210> 12	
<211> 30	
<212> DNA	
<213> Homo sapiens	
<400> 12	
tatgeggccg egagetgetg tgtcgcagae	30
<210> 13	
<211> 7	
<212> DNA	
<213> Homo sapiens	
•	
<400> 13	
rymaaya	7
<210> 14	
<211> 22	
<212> DNA	
<213> Homo sapiens	
AZIS Nome Express	
<400> 14	
tagtaaacac tctatcaatt gg	22
ragranded recured gg	
<210> 15	
<211> 20	
<211> 20 <212> DNA	
<213> Homo sapiens	
<400> 15	
gtccagtatc gtttacagcc	20
<210> 16	
<211> 21	
<212> DNA	
<213> Homo sapiens	
<400> 16	
cggattgtgt attggctgta c	21
<210> 17	
<211> 21	
<212> DNA	
<213> Homo sapiens	
<400> 17	
cggattctgt atcggctgta c	21

```
<210> 18
<211> 55
```

<212> DNA

<213> Homo sapiens

<400> 18

tatetgetge cetaaaatgt gtattecatg gaaatgtetg ceettetete egtac

55

<210> 19

<211> 518

<212> PRT

<213> Xenopus laevis

<400> 19

Met Arg Asp Pro Ser Ser Leu Tyr Ser Gly Phe Pro Ala Gly Ser Gln Tyr Glu Ser Val Glu Pro Pro Ser Leu Ala Leu Leu Ser Ser Ile Asp Gln Glu Gln Leu Pro Val Ala Thr Gly Gln Ser Tyr Asn His Ser Val 40 Gln Pro Trp Pro Gln Pro Trp Pro Pro Leu Ser Leu Tyr Arg Glu Gly Gly Thr Trp Ser Pro Asp Arg Gly Ser Met Tyr Gly Leu Ser Pro Gly Thr His Glu Gly Ser Cys Thr His Thr His Glu Gly Pro Lys Asp Ser 90 Met Ala Gly Asp His Thr Arg Ser Arg Lys Ser Lys Lys Lys Asn Tyr 100 105 His Arg Tyr Tyr Lys Pro Pro Tyr Ser Tyr Leu Ala Met Ile Ala Leu Val Ile Gln Asn Ser Pro Glu Lys Arg Leu Lys Leu Ser Gln Ile Leu 135 Lys Glu Val Ser Thr Leu Phe Pro Phe Phe Asn Gly Asp Tyr Met Gly 150 155 Trp Lys Asp Ser Ile Arg His Asn Leu Ser Ser Ser Asp Cys Phe Lys 165 170 Lys Ile Leu Lys Asp Pro Gly Lys Pro Gln Ala Lys Gly Asn Phe Trp 180 185 Thr Val Asp Val Ser Arg Ile Pro Leu Asp Ala Met Lys Leu Gln Asn 200 Thr Ala Leu Thr Arg Gly Gly Ser Asp Tyr Phe Val Gln Asp Leu Ala 215 220 Pro Tyr Ile Leu His Asn Tyr Lys Tyr Glu His Asn Ala Gly Ala Tyr 230 235 Gly His Gln Met Pro Pro Ser His Ala Arg Ser Leu Ser Leu Ala Glu 245 250 Asp Ser Gln Gln Thr Asn Thr Gly Gly Lys Leu Asn Thr Ser Phe Met 265 Ile Asp Ser Leu Leu His Asp Leu Gln Glu Val Asp Leu Pro Asp Ala 280 Ser Arg Asn Leu Glu Asn Gln Arg Ile Ser Pro Ala Val Ala Met Asn 295 Asn Met Trp Ser Ser Ala Pro Leu Leu Tyr Thr His Ser Lys Pro Thr 315 Arg Asn Ala Arg Ser Pro Gly Leu Ser Thr Ile His Ser Thr Tyr Ser 325 330 Ser Ser Ser Ser Ser Ile Ser Thr Ile Ser Pro Val Gly Phe Gln Lys 345 Glu Glu Glu Lys Ser Gly Arg Gln Thr Gln Arg Val Gly His Pro Ile

Lys Arg Ser Arg Glu Asp Asp Cys Ser Thr Thr Ser Ser Asp Pro Asp Thr Gly Asn Tyr Ser Pro Ile Glu Pro Pro Lys Lys Met Pro Leu Leu Ser Leu Asp Leu Pro Thr Ser Tyr Thr Lys Ser Val Ala Pro Asn Val Val Ala Pro Pro Ser Val Leu Pro Phe Phe His Phe Pro Arg Phe Thr Tyr Tyr Asn Tyr Gly Pro Ser Pro Tyr Met Thr Pro Pro Tyr Trp Gly Phe Pro His Pro Thr Asn Ser Gly Gly Asp Ser Pro Arg Gly Pro Gln Ser Pro Leu Asp Leu Asp Asn Met Leu Arg Ala Met Pro Pro Asn Lys Ser Val Phe Asp Val Leu Thr Ser His Pro Gly Asp Leu Val His Pro Ser Phe Leu Ser Gln Cys Leu Gly Ser Ser Gly Ser Pro Tyr Pro Ser Arg Gln Gly Leu Met